Effect of crossbreeding on the milk, fat and protein yields of Brown Swiss x Holstein hybrids- A meta-analysis

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Abstract

Due to the intensive selection the Holstein cattle breed has been submitted to, functional characteristics such as ease of calving and longevity have decayed over time. The use of crossbreeding with breeds that have not been so intensively selected has been suggested to combat these negative effects, as well as to improve the content of milk solids. The rearing of Holstein and Brown Swiss cows, as well as their hybrids, has been characterized by several publications. The aim of this study was to study the effect of crossbreeding in the milk, fat and protein yields of Brow Swiss x Holstein hybrid animals using existing literature. Nine papers were selected, and a meta-analysis was performed, comparing the average milk, fat, and protein yields of hybrid animals with those of purebred Holstein animals. The differences between the fat and protein yields were not found to be statistically significant ($p>0.05$), while the milk yield of purebred Holstein cows proved to be significantly higher than that of Brown Swiss hybrids ($p<0.05$). More recent studies and further analysis of other characteristics are necessary to reach more accurate conclusions.

Keywords: crossbreeding; Holstein; Brown Swiss; milk production; fat yield; protein yield

Introduction

The global milk production has drastically increased in the last 100 years, as illustrated by Figure 1. In 2020 alone, around 906 million tons of cow milk were produced (*FAOSTAT*, 2023), and an annual increase of 1.6% is to be expected in the next ten years (*OECD-FAO Agricultural Outlook 2020-2029*, 2020). Daily milk yields of 60 kilograms (kg) are not uncommon, and the record for highest milk yield by a Holstein cow was over 30 000 kg in one year, in 2006 (VandeHaar & St-Pierre, 2006).

This increase in animal productivity is due to an intensive selection, which in the past was purely based on phenotype, and in the present is facilitated by a deeper knowledge of genetics, and by breeding programs designed with the sole goal of increasing each animal's milk yield, whose effectiveness have increased greatly over time (Clay et al., 2020; Dechow et al., 2007; Hansen, 2000). However, this intensive selection has resulted in the decay of the functional characteristics of animals, such as the ease of calving, fertility, udder health, and longevity, as well as high inbreeding rates (Dezetter et al., 2019; El-Tarabany et al., 2016; Heringstad et al., 2003; Veerkamp et al., 2001). Due to its status as the most important breed in the dairy industry world-wide, the Holstein has been primarily affected by these changes, with the selection for high milk yield and larger body size impacting its overall health, longevity and functional characteristics (Hansen, 2000; Ma et al., 2019). Ma et al, found that, compared to a group of Holstein cows that had not been subject to any selection since 1964, modern cows had significantly lower fertility and immunity, due to the genes that are associated with those traits sharing chromosomes regions with those that impact milk production (Ma et al., 2019).

Not only has there been a general decline in these economically important characteristics in the Holstein breed, but there has also been a growing interest in the quantity of milk solids, such as protein and fat. This may threaten the competitivity of the Holstein animals on the market, seeing as other breeds might not produce as much total milk volume, but can have very high fat and protein yields, for example (Dezetter et al., 2017; Edwards et al., 2019).

To combat the negative impacts of selection in Holstein cows, some crossbreeding programs were designed to take advantage of other breeds that have a similar, yet lower, productivity, but that possess better functional characteristics, and different milk quality parameters (Sørensen et al., 2008). The Jersey and the Brown Swiss, for example, have a lower milk production, but greater protein and fat production than the Holstein (Auldist et al., 2004; de Marchi et al., 2007), which is known for a high milk production and lower protein yield (de Marchi et al., 2007; Macheboeuf et al., 1993).

Several studies were conducted with many breeds, particularly with the Jersey breed- These studies were the subject of a revision by LeChartier et al. in 2013 (LeChartier et al., 2013).

Considering that the Brown Swiss breed has a similar body size and milk production to the Holstein, and is not an uncommon breed to cross with the Holstein (El-Tarabany et al., 2016), this analysis aims to compile the literature's results concerning the crossbreeding of Holstein cows with Brown Swiss bulls, and to determine to effects of this crossbreeding on the animals' productivity.
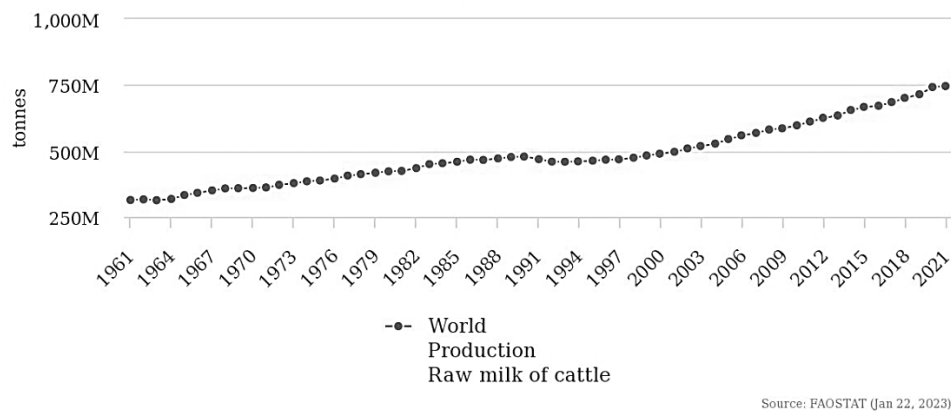

Figure 1. Annual, worldwide milk production (tons/year) in the last 60 years (*FAOSTAT*, **2023**).

Materials and Methods

A database was constructed from 9 studies (Table 1) that compared the productivity of Holstein cows with Brown Swiss x Holstein hybrids. The following variables were evaluated: milk yield (kg/d), fat in milk yield (kg/d) and protein in milk yield (kg/d).

To build this database, an online search was conducted with the B-On and Google Scholar search engines, with different combinations of the following keywords: 'holstein', 'brown swiss', 'crossbreeding', 'hybrid' and 'milk yield'. The references of found studies were also scanned for potential candidates. Patents and citations were filtered out from the results, as well as results in other languages than English. No timeframe was decided upon, the oldest study found being from 1974 and the most recent ones in 2017.

These search engines were first consulted in March 2020, and lastly in December 2022. Following this, papers with results in the desired units (kilograms or kilograms/day) were selected for the meta-analysis. Studies that did not explicitly present their results were not selected. Only studies with both purebred Holstein and Brown Swiss x Holstein populations were chosen. This process is illustrated in Figure 2.

One reviewer verified the validity of the papers' inclusion in the study. Data was manually collected from the reports by the same reviewer. Data in the preferred units (kg and kg/d) was directly utilized in the study, and data reported in other ways (standard errors and p-values) was transformed into workable datasets, as described further below. Neither of these processes were automated.

Papers were numbered chronologically to facilitate the creation of tables. It is of note that Study 1 (Brandt et al., 1974), Study 2 (Rincon et al., 1982), Study 3 (Dechow et al., 2007) and Study 9 (Endo et al., 2017) had two sets of data, which were then numbered 1.1, 1.2, 2.1, 2.2, 3.1, 3.2, 9.1 and 9.2, to indicate that these sets were treated separately.

The first paper (Brandt et al., 1974) also showed results for a group of Holstein x Brown Swiss animals (Brown Swiss dam and Holstein bull), which were not included in this analysis, to avoid any impact this difference might have. Study 5 (Blöttner et al., 2011) showed three datasets of three different lactations from the same animals. As the data referred to the same group, unlike the other studies where the data belonged to different animals, the data was combined using the following method,

$\Sigma x = \mu * n$

$\Sigma x^2 = SD^2(n-1) + ((\Sigma x)^2/n)$

t_n = sum of all n

t_x = sum of all Σx

t_{x2} = sum of all Σx^2

$n_c = t_n$

$\mu_c = t_x / t_n$

$SD_c = sqrt((t_{x2} - t_x^2/t_n) / (t_n - 1))$

Where n is the number of observations, SD is the standard deviation, n_c is the combined number of observations, μ_c is the combined average and SD_c is the combined standard deviation (Higgins et al., 2022).

To perform the meta-analysis, the averages and the standard deviations were used. Least Square Means (LSMs) were considered to be means. Four of the nine studies only reported the standard error, which was used to calculate the standard deviation (standard error multiplied by the square root of n). Two of the papers only presented the p-value, from which was calculated the t-value, and from this value the standard error was obtained. The previous calculations were repeated to obtain the standard deviation. Two of the other studies had none of these values, and thus they were assigned a standard deviation equal to that of the highest SD from another paper. This decreased their weight in the analysis (Higgins et al., 2019). The *metafor* package for RStudio (RStudio 2021.09.0+351 "Ghost Orchid" Release for Windows) was used to perform the statistical analysis and to create *forest plots* for each of the three variables, as well as calculating their p-values. *Metafor* utilizes a random effects model with the following equation:

$y_i = \mu + u_i + \varepsilon_i$

where $u_i \sim N (0, \tau^2)$

and $\varepsilon_i \sim N (0, v_i)$.

This model assumes that the chosen studies are a random sample from a larger population and provides an unconditional inference of the analyzed effects (Viechtbauer, 2010).

Metafor also provides tools to evaluate bias: in this meta-analysis, the funnel plots provided were used to assess any possible publication bias.

Table 1. Studies used for meta-analysis.

Study No.	Title	Author	Year
1 1.2	Production of Milk and Milk Constituents by Brown Swiss, Holsteins, and their Crossbreds	Brandt et al.	1974
2.1 2.2	Estimation of Genetic Effects on Milk Yield and Constituent Traits in Crossbred Dairy Cattle	Rincon et al.	1982
3.1 3.2	Milk, Fat, Protein, Somatic Cell Score, and Days Open Among Holstein, Brown Swiss, and Their Crosses	Dechow et al.	2007
4	Crossbreeding in dairy cattle: International trends and results from crossbreeding data in Germany	Swalve	2007
5	A comparison between purebred Holstein and Brown Swiss x Holstein cows for milk production, somatic cell score, milking speed, and udder measurements in the first 3 lactations	Blöttner et al.	2011
6	Milk quality, coagulation properties, and curd firmness modelling of purebred Holsteins and first- and second-generation crossbred cows from Swedish Red, Montbéliarde, and Brown Swiss bulls	Malchiodi et al.	2014
7	Production and health performance of Holstein, Brown Swiss and their crosses under subtropical environmental conditions	M. El-Tarabany et al.	2016
8	Impact of crossbreeding Holstein and Brown Swiss cows on milk yield, composition, and fatty acid profiles in subtropics	M. El-Tarabany et al.	2018
9.1 9.2	Comparison of productive and reproductive performance and hair cortisol levels between Brown Swiss cross-bred and Holstein cows housed in the same barn	Endo et al.	2017
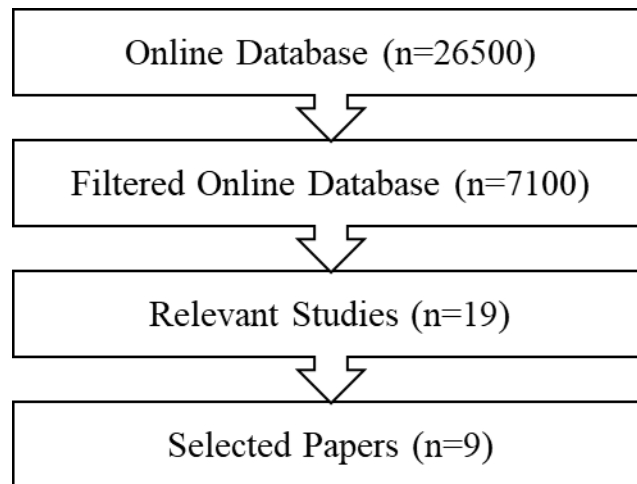
Figure 2. Paper selection process.

Results

Results are shown in Figures 3, 4, and 5, while Table 2 reports on the variables' p-values. Significance was declared at p<0.05. In relation to daily milk yield, a portion of studies cross the line of null effect (vertical axis), and therefore show no statistically significant result, while others do not cross it, which indicates statistically significant results. As for the daily fat yield in milk, only two studies show a statistically significant result (El-Tarabany et al., 2018; Endo et al., 2017).

Table 2. Calculated p-value for each variable; * indicates significance.

Variable	p-value
Daily milk yield	0.0008*
Daily fat yield	0.5702
Daily protein yield	0.0971

Forest Plot

Study 1   1.99 [-0.26, 4.24]
Study 2   -0.34 [-2.38, 1.70]
Study 3   0.93 [-0.64, 2.50]
Study 4   0.94 [-0.00, 1.88]
Study 5   0.46 [0.00, 0.92]
Study 6   0.19 [-3.15, 3.53]
Study 7   0.78 [-0.59, 2.15]
Study 8   4.53 [1.88, 7.18]
Study 9   0.75 [0.21, 1.29]
Study 10   1.80 [0.47, 3.13]
Study 11   5.37 [3.05, 7.68]
Study 12   6.67 [2.42, 10.91]

RE Model   1.60 [0.67, 2.54]

-5   0   5   10   15
Mean Difference
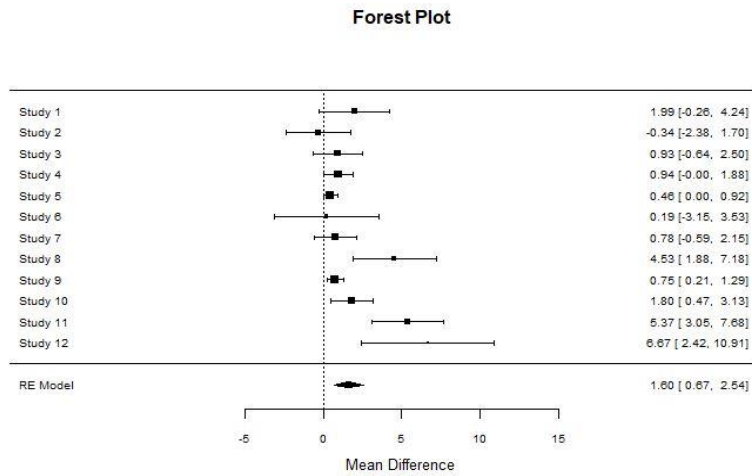
Fig 3. Forest plot of daily milk yield.

Forest Plot

Study 1   0.04 [-0.05, 0.13]
Study 2   -0.05 [-0.14, 0.04]
Study 3   0.00 [-0.06, 0.06]
Study 4   -0.06 [-0.12, -0.00]
Study 5   -0.09 [-0.18, 0.00]
Study 6   -0.03 [-0.14, 0.08]
Study 7   -0.01 [-0.07, 0.05]
Study 8   0.12 [0.03, 0.21]
Study 10   0.02 [-0.06, 0.10]
Study 11   0.12 [0.04, 0.20]
Study 12   0.15 [-0.00, 0.30]

RE Model   0.01 [-0.03, 0.06]

-0.2   -0.1   0   0.1   0.2   0.3
Mean Difference
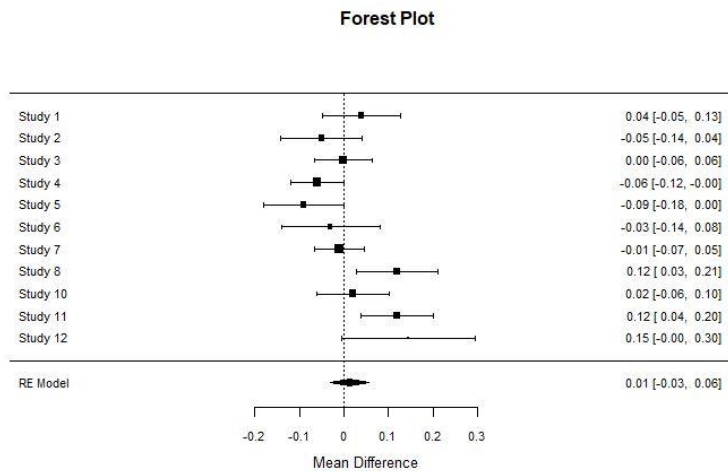
Fig 4. Forest plot of daily fat yield.

Forest Plot

Study 1   0.06 [-0.02, 0.14]
Study 2   -0.02 [-0.10, 0.06]
Study 3   0.01 [-0.04, 0.06]
Study 4   -0.02 [-0.05, 0.01]
Study 5   -0.04 [-0.08, -0.00]
Study 6   -0.03 [-0.11, 0.05]
Study 7   -0.01 [-0.05, 0.03]
Study 8   0.15 [-0.00, 0.30]
Study 10   0.08 [0.03, 0.13]
Study 11   0.21 [0.13, 0.29]
Study 12   0.26 [0.11, 0.41]

RE Model   0.05 [-0.01, 0.10]

-0.2 -0.1   0   0.1 0.2 0.3 0.4 0.5
Mean Difference
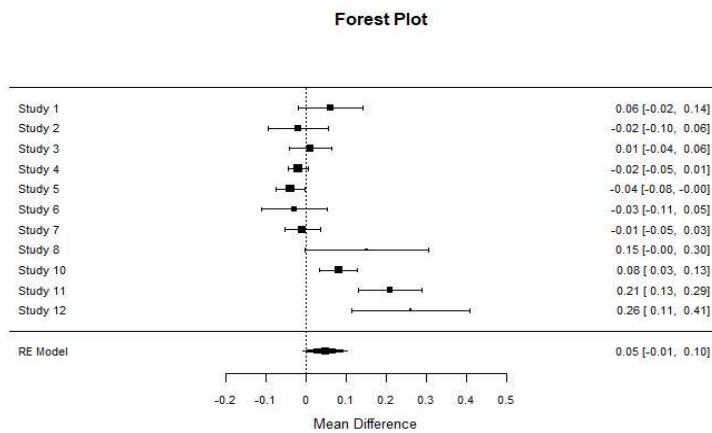
Fig 5. Forest plot of daily protein yield.

Discussion

Of the three studied variables, the differences between the fat and milk yield of Holstein purebreds and Brown Swiss x Holstein hybrid cows were not found to be statistically significant ($p>0.05$). However, the difference between their daily milk yield was ($p<0.05$), with the purebred cows producing more milk per day, on average. These results, taken without context, would imply that it would not be profitable to crossbreed Holstein and Brown Swiss animals, since their productivity is decreased, and the differences in fat and protein content are not significant. However, this analysis only focuses on the daily milk, protein, and fat yields. There may be other variables that could prove interesting to farmers, that were not included in the analysis, such as time between calving, calving ease and longevity.

As Weigel & Barlass reported in 2003, producers found that Holstein purebred cows had a higher milk yield indeed, but their milk was poorer in solids, and they had a higher rate of involuntary culling (Weigel & Barlass, 2003). Hybrids were also perceived to have a higher conception rate, a higher calving ease, and slightly lower calf mortality. El-Tarabany and Nasr found that Brown Swiss cows and first-generation crosses with Holstein displayed higher conception and pregnancy rates, shorter calving intervals and lower incidence of metritis than Holstein cows and backcrosses (El-Tarabany & Nasr, 2015).

Furthermore, the number of papers found and used is limited, which may influence the results, and some papers, such as Brandt et al., 1974, and Rincon et al., 1982, are quite old, having been published over 40 years ago. As mentioned in the introduction, dairy breeds' productivity has sharply increased since the 60s, which may once more have affected the analysis' results. Meta-analysis depends heavily on the quantity and quality of data published, so one must take into consideration the amount of literature one can find, as well as its age and scientific rigor (Shorten & Shorten, 2013).

Publication bias is yet another factor that must be considered. Studies that show significant effects are much more likely to be published than their counterparts (Sterne et al., 2001). Funnel plots may be used to scan for publication bias, as an asymmetric plot may indicate possible bias; however, one should consider that the lower the number of studies, the lower the power of the test (Higgins et al., 2022; Lau et al., 2006). In Figures 6, 7, and 8, the funnel plots created by the *metaphor* package for each variable can be seen. The plots are not symmetric, which could indicate publication bias, even considering the low number of studies. This must be taken into account when considering the analysis' result.

Furthermore, several assumptions that possibly affected the results were also used in the methodology: for the papers lacking data (standard deviation, standard error or p-values), the highest standard deviation from the other studies was used, decreasing their weight in the analysis. This conservative estimate may have altered the significance of certain variables, and it is possible that the real significance is different.
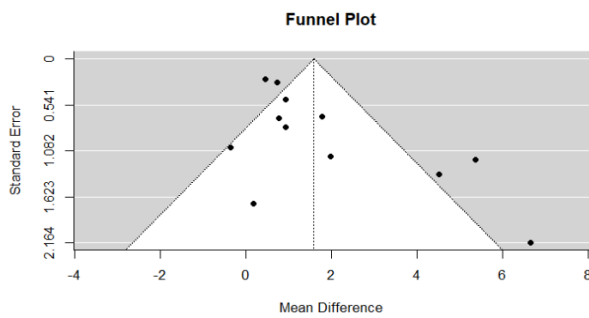

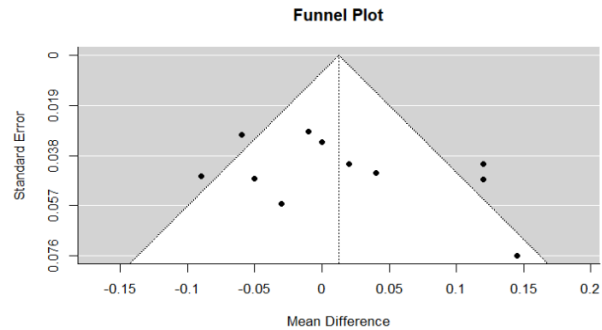**Fig 6.** Funnel plot of daily protein yield.

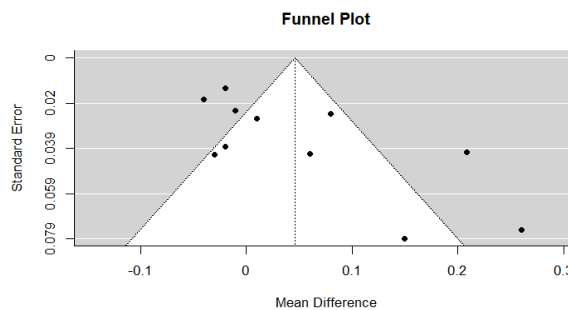**Fig 7.** Funnel plot of daily protein yield.

Fig 8. Funnel plot of daily protein yield.

Conclusions

There was no significant difference found between the daily protein and fat yield of purebred Holstein animals, and Brown Swiss x Holstein crossbred animals. However, the daily milk yield of Holsteins was found to be significantly higher than that of the crossbreds. Despite this possibly indicating that crossbred animals are not as worthwhile as purebred Holsteins, this analysis did not consider different factors that could influence a producer's decision to obtain crossbred animals, such as longevity, health, ease of calving, conception rate and calf mortality. For a more thorough analysis, more factors should be taken into consideration, and more recent literature should be used.

Declaration of Interest

The authors declare no conflict of interest.

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